

Figure 1 illustrates the classification of 1000 randomly selected genes into 10 clusters based on 10 different criteria. The criteria are: 1. Gene expression level, 2. Gene length, 3. Gene density, 4. Gene conservation, 5. Gene function, 6. Gene structure, 7. Gene location, 8. Gene interaction, 9. Gene annotation, and 10. Gene family. The flowchart shows how these criteria are used to group genes into clusters, with some clusters being further subdivided. For example, Cluster 1 (Gene expression level) is subdivided into 10 sub-clusters. Cluster 2 (Gene length) is subdivided into 10 sub-clusters. Cluster 3 (Gene density) is subdivided into 10 sub-clusters. Cluster 4 (Gene conservation) is subdivided into 10 sub-clusters. Cluster 5 (Gene function) is subdivided into 10 sub-clusters. Cluster 6 (Gene structure) is subdivided into 10 sub-clusters. Cluster 7 (Gene location) is subdivided into 10 sub-clusters. Cluster 8 (Gene interaction) is subdivided into 10 sub-clusters. Cluster 9 (Gene annotation) is subdivided into 10 sub-clusters. Cluster 10 (Gene family) is subdivided into 10 sub-clusters. The flowchart also shows the relationship between the clusters and the criteria, with some clusters being more closely related to certain criteria than others.

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